

SEQUENCE LISTING

(1) GENERAL INFORMATION

- (i) APPLICANT: Lal, Preeti  
Corley, Neil C.
- (ii) TITLE OF THE INVENTION: HUMAN SHORT CHAIN DEHYDROGENASE
- (iii) NUMBER OF SEQUENCES: 3
- (iv) CORRESPONDENCE ADDRESS:
  - (A) ADDRESSEE: Incyte Pharmaceuticals, Inc.
  - (B) STREET: 3174 Porter Dr.
  - (C) CITY: Palo Alto
  - (D) STATE: CA
  - (E) COUNTRY: USA
  - (F) ZIP: 94304
- (v) COMPUTER READABLE FORM:
  - (A) MEDIUM TYPE: Diskette
  - (B) COMPUTER: IBM Compatible
  - (C) OPERATING SYSTEM: DOS
  - (D) SOFTWARE: FastSEQ for Windows Version 2.0
- (vi) CURRENT APPLICATION DATA:
  - (A) APPLICATION NUMBER: To Be Assigned
  - (B) FILING DATE: Filed Herewith
  - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
  - (A) APPLICATION NUMBER:
  - (B) FILING DATE:
- (viii) ATTORNEY/AGENT INFORMATION:
  - (A) NAME: Billings, Lucy J.
  - (B) REGISTRATION NUMBER: 36,749
  - (C) REFERENCE/DOCKET NUMBER: PF-0475 US
- (ix) TELECOMMUNICATION INFORMATION:
  - (A) TELEPHONE: 650-855-0555
  - (B) TELEFAX: 650-845-4166
  - (C) TELEX:

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 313 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (vii) IMMEDIATE SOURCE:
  - (A) LIBRARY: PROSNOT01
  - (B) CLONE: 356351
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Met	Ala	Ala	Pro	Met	Asn	Gly	Gln	Val	Cys	Val	Val	Thr	Gly	Ala	Ser	1	5	10	15
Arg	Gly	Ile	Gly	Arg	Gly	Ile	Ala	Leu	Gln	Leu	Cys	Lys	Ala	Gly	Ala	20	25	30	
Thr	Val	Tyr	Ile	Thr	Gly	Arg	His	Leu	Asp	Thr	Leu	Arg	Val	Val	Ala	35	40	45	
Gln	Glu	Ala	Gln	Ser	Leu	Gly	Gln	Cys	Val	Pro	Val	Val	Cys	Asp		50	55	60	
Ser	Ser	Gln	Glu	Ser	Glu	Val	Arg	Thr	Leu	Phe	Glu	Gln	Val	Asp	Arg	65	70	75	80
Glu	Gln	Gln	Gly	Arg	Leu	Asp	Val	Leu	Val	Asn	Asn	Ala	Tyr	Ala	Gly	85	90	95	
Val	Gln	Thr	Ile	Leu	Asn	Thr	Arg	Asn	Lys	Ala	Phe	Trp	Glu	Thr	Pro	100	105	110	
Ala	Ser	Met	Trp	Asp	Asp	Ile	Asn	Asn	Val	Gly	Leu	Arg	Gly	His	Tyr	115	120	125	
Phe	Cys	Ser	Val	Tyr	Gly	Ala	Arg	Leu	Met	Val	Pro	Ala	Gly	Gln	Gly	130	135	140	
Leu	Ile	Val	Val	Ile	Ser	Ser	Pro	Gly	Ser	Leu	Gln	Tyr	Met	Phe	Asn	145	150	155	160
Val	Pro	Tyr	Gly	Val	Gly	Lys	Ala	Ala	Cys	Asp	Lys	Leu	Ala	Ala	Asp	165	170	175	
Cys	Ala	His	Glu	Leu	Arg	Arg	His	Gly	Val	Ser	Cys	Val	Ser	Leu	Trp	180	185	190	
Pro	Gly	Ile	Val	Gln	Thr	Glu	Leu	Lys	Glu	His	Met	Ala	Lys	Glu		195	200	205	
Glu	Val	Leu	Gln	Asp	Pro	Val	Leu	Lys	Gln	Phe	Lys	Ser	Ala	Phe	Ser	210	215	220	
Ser	Ala	Glu	Thr	Thr	Glu	Leu	Ser	Gly	Lys	Cys	Val	Val	Ala	Leu	Ala	225	230	235	240
Thr	Asp	Pro	Asn	Ile	Leu	Ser	Leu	Ser	Gly	Lys	Val	Leu	Pro	Ser	Cys	245	250	255	
Asp	Leu	Ala	Arg	Arg	Tyr	Gly	Leu	Arg	Asp	Val	Asp	Gly	Arg	Pro	Val	260	265	270	
Gln	Asp	Tyr	Leu	Ser	Leu	Ser	Ser	Val	Leu	Ser	His	Val	Ser	Gly	Leu	275	280	285	
Gly	Trp	Leu	Ala	Ser	Tyr	Leu	Pro	Ser	Phe	Leu	Arg	Val	Pro	Lys	Trp	290	295	300	
Ile	Ile	Ala	Leu	Tyr	Thr	Ser	Lys	Phe								305	310		

## (2) INFORMATION FOR SEQ ID NO:2:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1387 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (vii) IMMEDIATE SOURCE:

- (A) LIBRARY: PROSNOT01
- (B) CLONE: 356351

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

CTAACTTTGG	CCTGGGACTC	TGCCCCCTCTA	CCTCAGCACA	GAATCGCCCC	GGGTCCTACT	60
ACAGAATCAA	TCCTTGAACA	CTGCCTCCAC	GTCGCCGGCT	CAATCTGGGC	GAGAACCCAG	120
ACTTCCACCG	CAGCCCCGCA	ATCTGCAGAC	CTCAGCGGCA	GCGCAGGTGG	CAGACCTGCC	180
TCCTTTGCCT	GTGAGTCATG	GCAGCTCCCA	TGAATGGCCA	AGTGTGTGTG	GTGACTGGTG	240

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CCTCCAGGGG TATTGGCCGT GGCATTGCCT TGCAGCTCTG CAAAGCAGGC GCCACAGTTT 300
ACAACACTGG CCGCCATCTG GACACCCTTC GCGTTGTTGC TCAGGAGGCA CAATCCCTCG 360
GGGGCCAATG TGTGCCTGTG GTGTGCGATT CAAGCCAGGA GAGTGAAGTG CGAACGCTGT 420
TTGAGCAAGT GGATCGGGAA CAGCAAGGGC GTCTAGATGT GCTGGTCAAC AATGCTTATG 480
CAGGGGTCCA GACGATCCTG AACACCAGGA ATAAGGCATT CTGGGAAACC CCTGCCTCCA 540
TGTGGGATGA TATCAACAAC GTCGGACTCA GAGGCCACTA CTTTTGCTCA GTGTATGGGG 600
CACGGCTGAT GGTACCAGCT GGCCAGGGGC TCATCGTGGT CATCTCCTCC CCAGGAAGCC 660
TGCAGTATAT GTTCAATGTC CCCTATGGTG TGGGCAAAGC TGCCTGTGAC AAGCTGGCTG 720
CTGACTGTAC CCACGAGCTG CGGCGCCATG GGGTCAGCTG TGTGTCTCTG TGGCCGGGGA 780
TTGTGTCAGC AGAAGTGCTG AAGGAGCATA TGGCAAAGGA GGAGGTCCTG CAGGATCCTG 840
TGTTGAAGCA GTTCAAATCA GCCTTCTCAT CTGCAGAAAC CACAGAATTG AGTGGCAAAT 900
GTGTGGTGGC TTTGGCAACA GATCCCAATA TCCTGAGCCT GAGTGGTAAG GTGCTGCCAT 960
CCTGTGACCT TGCTCGACGC TATGGCCTTC GGGATGTGGA CGGCCGCCCC GTCCAAGACT 1020
ATTTGTCTTT GAGCTCTGTT CTCTCACACG TGTCCGGCCT GGGCTGGCTG GCCTCCTACC 1080
TGCCCTCCTT CCTCCGTGTG CCAAGTGGA TTATTGCCCT CTACACTAGC AAGTTCTAAC 1140
CCTCCTGGTC TGACACTACG TCTCTGCTTG TCTTCTCATT TGGACTTGGT GGTTTCGTCT 1200
GTCTCAGTGA AACAGCAGCC TTTCTTGTTC ACCCATACCC TTGATATGAA GAGAAGCCCT 1260
CTGCTGTGTG TCCGTGGTGA GTTCTGGGGT GCGCCTAGGT CCCTTCTTTG TGCCTTGCTT 1320
TTCCTTGTC TTCTTTTAC TTTTTCCTT AGTATTGAAA AATGCTCTTG GAGCTAATAA 1380
AAGTCTA 1387

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## (2) INFORMATION FOR SEQ ID NO:3:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 323 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (vii) IMMEDIATE SOURCE:

- (A) LIBRARY: GenBank
- (B) CLONE: 2315796

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

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Met Gly Val Ile Leu Gln Asp Gln Val Ala Leu Val Thr Gly Ala Ser
 1           5           10           15
Arg Gly Ile Gly Arg Gly Ile Ala Leu Gln Leu Gly Glu Ala Gly Ala
 20           25           30
Thr Val Tyr Ile Thr Gly Arg Arg Pro Glu Leu Ser Asp Asn Phe Arg
 35           40           45
Leu Gly Leu Pro Ser Leu Asp Tyr Val Ala Lys Glu Ile Thr Ser Arg
 50           55           60
Gly Gly Lys Gly Ile Ala Leu Tyr Val Asp His Ser Asn Met Thr Glu
 65           70           75           80
Val Lys Phe Leu Phe Glu Lys Ile Lys Glu Asp Glu Glu Gly Lys Leu
 85           90           95
Asp Ile Leu Val Asn Asn Val Tyr Asn Ser Leu Gly Lys Ala Thr Glu
100          105          110
Met Ile Gly Lys Thr Phe Phe Asp Gln Asp Pro Ser Phe Trp Asp Asp
115          120          125
Ile Asn Gly Val Gly Leu Arg Asn His Tyr Tyr Cys Ser Val Tyr Ala
130          135          140
Ala Arg Met Met Val Glu Arg Arg Lys Gly Leu Ile Val Asn Val Gly
145          150          155          160
Ser Leu Gly Gly Leu Lys Tyr Val Phe Asn Val Ala Tyr Gly Ala Gly
165          170          175
Lys Glu Ala Leu Ala Arg Met Ser Thr Asp Met Ala Val Glu Leu Asn
180          185          190

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# SECRET